

FIGURE 1

cDNA sequence of wild type amFP486

ATGGCTCTTCAAACAAGTTATCGGAGATGACATGAAAATGACCTACCATAATGGATG
 GCTGTGTCATGGCATTACTTACCGTCAAAGGTGAAGGCAACGGGAAGCCATACGA
 AGGGACGCAGACCTCGACTTTAAAGTCACCATGGCCAACGGTGGGCCCTGCATT
 TCCCTTGACATACTATCTACAGTGTCAAGTATGAAATCGATGCTTACTGCGTATC
 CTACCACTATGCCGACTATTCAAACAAGCATTCTGACGGAATGTATGAAAG
 GACTTTACCTATGAAGATGGAGGAGTTGCTACAGCCAGTTGGGAAATAAGCCTAAA
 GGCAACTGCTTGAGCACAAATCCACGTTCATGGAGTGAACCTCCTGCTGATGGAC
 CTGTGATGGCGAAGATGACAACGGGACCCATCTTGAGAAAATGACTGTCTG
 CGATGGAATATTGAAGGGTGATGTCACCGCGTTCATGCTGCAAGGAGGTGGCAAT
 TACAGATGCCAATTCCACACTTCTTACAAGACAAAAAACCGGTGACGATGCCACCAA
 ACCATGCGGTGGAACATCGCATTGCGAGGACCGACCTGACAAAGGTGGCAACAGTGT
 TCAGCTGACGGAGCACGCTGTTGCACATATAACCTCTGTTGTCCCTTTC (SEQ ID
 NO:01)

amino acid sequence of wild type amFP486

MALSNKFIGD DMKMTYHMDG CVNGHYFTVK GEGNGKPYEG TQTSTFKVTM ANGGPLAFSF
 DILSTVFKYG NRCFTAYPTS MPDYFKQAFP DGMSYERTFT YEDGGVATAS WEISLKGNCF
 EHKSTFHGVN FPADGPVMAK MTTGWDPSFE KMTVCDGILK GDVTAFLMLQ GGGNYRCQFH
 TSYKTKKPVT MPPNHAVEHR IARTDLDKGG NSVQLTEHAV AHITSVVPF

(SEQ ID NO:02)

Figure 2

cDNA sequence of wild type cFP484

TATAGGANCATNNGGGNGATTGGGGTCAAAGCATTGTAACCAACGCAGATAACCCCCAG
 TGGTNTCAAACGCAGANAACGGAACATTGAAAATTGANTNTAAGGAGGAAGGAA
 TCGGGAGTAAAGTTGCGAGAAACTGAAAAAATGAAGTGAAATTGTGTTCTGCCTGTCC
 TTCTGGTCCTCGCCATCACAAACGCAACATTGAGAAACAGAGGCTGACTTAGAA
 GAGAAGACATTGAGAATACCAAAAGCTCTAACACCATTGGGTGTGATTAAACCAGACATG
 AAGATTAAGCTGAAGATGGAAGGAATGTAACGGCATGCTTGTGATCGAAGGAGAA
 GGAGAAGGAAAGCCTAACGATGGGACACACACTTAAACCTGGAAGTGAAGGAAGGTGCG
 CCTCTGCCTTTCTTACGATATCTTGTCAAACGCGTCCAGTACGGAAACAGAGCATTG
 ACAAAATACCCAGACGATAGCAGACTATTCAAGCAGTCGTTCCGAGGGATATTCC
 TGGGAAAGAACCATGACTTTGAAGACAAAGCATTGTCAAAGTGAAGTACATAAGC
 ATGGAGGAAGACTCCTTATCTATGAAATTGTTGATGGGATGAACCTTCCTCCCAAT
 GGTCCGGTTATGCAGAAAAAAACTTGAAGTGGGAACCATCCACTGAGATTATGTACGTG
 CGTGATGGAGTGTGGTCGGAGATATTAGCATTCTCTGTTGCTGGAGGGAGGTGCCAT
 TACCGATGTGACTTCAAAAGTATTACAAGAAAAAAAGTTGTCAAATTGCCAGACTAT
 CACTTGTGGACCATCGCATTGAGATCTTGAACCATGACAAGGATTACAACAAAGTAACG
 CTGTATGAGAATGCAGTTGCTCGCTATTCTTGCTGCCAAGTCAGGCCTAGACAACAAGG
 ATACTGAAAACATATTGTCTGAGGGTTGTGTTTTAAAAGACATCAGCTCAGCA
 TTCGTTAGTTGTAACAAAAAATAGCTTAATTGGGGATTAATCATAGGGATTG
 TTTTAGTAATCATTGCTTAATAAAAGTGCCTG (SEQ ID NO:03)

amino acid sequence of wild type cFP484

M	K	C	K	F	V	F	C	L	S										
F	L	V	L	A	I	T	N	A	N	I	F	L	R	N	E	A	D	L	E
E	K	T	L	R	I	P	K	A	L	T	T	M	G	V	I	K	P	D	M
K	I	K	L	K	M	E	G	N	V	N	G	H	A	F	V	I	E	G	E
G	E	G	K	P	Y	D	G	T	H	T	L	N	L	E	V	K	E	G	A
P	L	P	F	S	Y	D	I	L	S	N	A	F	Q	Y	G	N	R	A	L
T	K	Y	P	D	D	I	A	D	Y	F	K	Q	S	F	P	E	G	Y	S
W	E	R	T	M	T	F	E	D	K	G	I	V	K	V	K	S	D	I	S
M	E	E	D	S	F	I	Y	E	I	R	F	D	G	M	N	F	P	P	N
G	P	V	M	Q	K	K	T	L	K	W	E	P	S	T	E	I	M	Y	V
R	D	G	V	L	V	G	D	I	S	H	S	L	L	E	G	G	G	H	
Y	R	C	D	F	K	S	I	Y	K	A	K	K	V	V	K	L	P	D	Y
H	F	V	D	H	R	I	E	I	L	N	H	D	K	D	Y	N	K	V	T
L	Y	E	N	A	V	A	R	Y	S	L	L	P	S	Q	A	(SEQ ID NO:04)			

Figure 3

cDNA sequence of zFP506

```
ATGGCTCAGTCAAAGCACGGCTAACAAAAGAAATGACAATGAAATACCGTATGGAAGGGTGC
GTCGATGGACATAAATTGTGATCACGGGAGAGGGCATTGGATATCCGTTCAAAGGGAAACAG
GCTATTAATCTGTGTGGTCAAGGTGGACCATTGCCATTGCCAAGACATATTGTCAGCT
GCCTTATGTACGGAAACAGGGTTTCACTGAATATCCTCAAGACATAGCTGACTATTCAAG
AACTCGTGTCTGCTGGTTATACATGGGACAGGTCTTCTCTTGAGGATGGAGCAGTTGC
ATATGTAATGCAGATAAACAGTGAGTGTGAAGAAAATGCATGTATCATGAGTCAAATT
TATGGAGTGAATTTCTGCTGATGGACCTGTGATGAAAAAGATGACAGATAACTGGGAGCCA
TCCTCGAGAAGATCATACCACTAAGCAGGGATATTGAAAGGGATGTCATGTAC
CTCCTTCTGAAGGATGGTGGCGTTACGGTCCAATTGACACAGTTACAAAGCAAAGTCT
GTGCCAAGAAAGATGCCGGACTGGCACTTCATCCAGCATAAGCTACCCGTGAAGACCGCAGC
GATGCTAAGAATCAGAAATGGCATTGACAGAACATGCTATTGCATCCGGATCTGCATTGCC
(SEQ ID NO:05)
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amino acid sequence of zFP506

```
MAQSKHGLTK EMTMKYRMEG CVDGHKFVIT GEGIGYPFKG KQAINLCVVE GGPLPFAEDI LSAAFNYGNR VFTEYPQDIA
DYFKNSCPAG YTWDRSFLFE DGAVCICNAD ITVSVEENCM YHESKFYGVN FPADGPVMKK MTDNWEPSCE KIIPVPKQGI
LKGDVSMYLL LKDGGRLRCQ FDTVYKAKSV PRKMPDWHFI QHKLTREDRS DAKNQKWLH EHAIASGSAL P
(SEQ ID NO:06)
```

Figure 4

cDNA sequence of zFP538

gagttgagtt tctcgacttc agttgtatca attttggggc atcaagcgat ctatTTcaa
 catggctcat tcaaaggc acg gtctaaaaga agaaatgaca atgaaatacc acatggagg
 gtgcgtcaac ggacataaaat ttgtgatcac gggcgaaggc attggatatac cgttcaaagg
 gaaacagact attaatctgt gtgtgatcga agggggacca ttgccattt ccgaagacat
 attgtcagct ggcttaagt acggagacag gatttcaact gaatatcctc aagacatagt
 agactatttc aagaactcgt gtcctgctgg atatacatgg ggcaggctt ttctcttga
 ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat
 ttatcataag agcatattta atggaatgaa tttcctgtc gatggacctg tgatgaaaaa
 gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcagggat
 actgaaaggg gatgtctcca tgtacccct tctgaaggat ggtggcggtt accgggtgcc
 gttcgacaca gtttacaaag caaagtctgt gccaaagtaag atgcccggagt ggcacttcat
 ccagcataag ctctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac
 agagcatgtc attgcattcc cttctgcctt ggcctgataa gaatgttagt ccaacattt
 aatgcatgtc cttgtcaattt attctgtataa aaatgttagt gagttgaaaaa cagacaagta
 caaataaaagc acatgtaaat cgtct (SEQ ID NO:07)

amino acid sequence of zFP538

Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys
 Tyr His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr
 Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn
 Leu Cys Val Ile Glu Gly Pro Leu Pro Phe Ser Glu Asp Ile
 Leu Ser Ala Gly Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr
 Pro Gln Asp Ile Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly
 Tyr Thr Trp Gly Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Ile
 Cys Asn Val Asp Ile Thr Val Ser Val Lys Glu Asn Cys Ile Tyr
 His Lys Ser Ile Phe Asn Gly Met Asn Phe Pro Ala Asp Gly Pro
 Val Met Lys Lys Met Thr Thr Asn Trp Glu Ala Ser Cys Glu Lys
 Ile Met Pro Val Pro Lys Gln Gly Ile Leu Lys Gly Asp Val Ser
 Met Tyr Leu Leu Lys Asp Gly Gly Arg Tyr Arg Cys Gln Phe
 Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys Met Pro Glu
 Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg Ser Asp
 Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala Phe
 Pro Ser Ala Leu Ala (SEQ ID NO:08)

FIGURE 5

cDNA sequence of dsFP483

ACGGTCAGGGACACGGTACCCACTTGGTATTCTAACAAAATGAGTTGGTCCAAGAGTG
TGATCAAGGAAGAATGTTGATCGATCTCATCTGGAAGGAACGTTCAATGGGCACTACT
TTGAAATAAAGGCAAAGGAAAGGGAAGCCTAATGAAGGCACCAATACCGTCACGCTCG
AGGTTACCAAGGGTGGACCTCTGCCATTGGTTGCATATTTGTGCCACAATTTCAGT
ATGGAAACAAGGCATTGTCACCACCCGTACGACATACCTGATTATCTAAAGCTGTCAT
TTCCGGAGGGATATACATGGGAACGGTCATGCACCTTGAAGACGGTGGCTGTGTTGTA
TCACCAATGATATCAGTTGACAGGCAACTGTTCAACTACGACATCAAGTTCACTGGCT
TGAACCTTCCTCCAAATGGACCCGGTGTGCAGAAGAAGACAACGGCTGGGAACCGAGCA
CTGAGCGTTGTATCCTCGTGTGGCGTGTGATAGGAGACATCCATCATGCTCTCACAG
TGGAAAGGAGGTGGTCAATTACGTATGTGACATTAAACTGTTACAGGGCCAAGAAGCCCG
TAAAGATGCCAGGGTATCACTATGTTGACACCAAACGGTTATAAGGAGCAACGACAAG
AATTGAAAGTGTGAGGAGCATGAAATGCCGTTGCACGCCACCATCCGCTCCAAAGCC
AATGAAAGCTTAAGTAAAGCAAAAGGTGACGAGGCATGATAGTATGACATGATAGTATGA
CATGATAGTATGACATGATAGTAAAGAATTGTAAGCAAAAGGCTTGCTTATTAAACTGT
AATTGAAAAC (SEQ ID NO: 09)

amino acid sequence of dsFP483

FIGURE 6

cDNA sequence of drFP583

ATGAGGTCTTCCAAGAATGTTATCAAGGAGTCATGAGGTTAACGGTCATGGAAAGGAACGGTCAATGGGCACGAGT
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGCTAACGGTAACCAAGGGGGGACC
 TTTGCCATTGCTGGATATTTGTCACCACAATTCACTGAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATA
 CCAGACTATAAAAAGCTGCTTCTGAAGGATTAAATGGGAAAGGGTCATGAACCTTGAAAGACGGTGGCGTCGTTA
 CTGTAACCCAGGATTCCAGTTGCAAGGATGGCTGTTCATCTACAAGGTCAAGTTCACTGGCGTGAACCTTCCTCCGA
 TGGACCTGTTATGCAAAGAACAAATGGGCTGGGAAGGCCAGCACTGAGCCTTGTATCCTCGTGAATGGCGTGTGAAA
 GGAGAGATTCTAAGGCTCTGAAGCTAACAGGGTCACTATGTTGACTCCAAACTGGATATAACAAGCCACAACGAAGACTATACATCGT
 AGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGATATAACAAGCCACAACGAAGACTATACATCGT
 TGAGCAGTATGAAAGAACCGAGGGACGCCACCATCTGTTCTTAA (SEQ ID NO:11)

cDNA sequence of drFP583.1

GTCCTCCCAGCAGTGGTATCAACGCAGAGTACGGGGAGTTCAAGCCAGTGACGGT
 CAGTGACAGGGTGAGCCACTTGGTATACCAACAAATGAGGTCTTCCAAGAATGTTA
 TCAAGGAGTTCATGAGGTTAACGGTCATGGAAAGGAACGGTCAATGGGCACGAGT
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGC
 TTAAGGTAACCAAGGGGGACCTTGCCTTGCATGGGATATTTGTCACCACAAT
 TTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACAGACTATAAAA
 AGCTGTCATTCTGAAGGATTAAATGGGAAAGGGTCATGAACCTTGAAAGACGGTG
 GCGTCGTTACTGTAACCCAGGATTCAGGTTGCAGGATGGCTGTTCATCTACAAGT
 CAAGTTCATGGCGTTGAACCTTCCCTTGCGATGGACCTGTTATGCAAAGAACAA
 TGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTGAATGGCGTGTGAAAGGAG
 AGATTCTAAGGCTCTGAAGCTGAAAGACGGTGGTCACTACCTAGTTGAATTCAA
 GTATTTCATGGCAAAGAACGCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCA
 AACTGGATATAACAAGCCACAACGAAGACTATACAATGTTGAGCAGTATGAAAGAA
 CCGAGGGACGCCACCCTGTTCTTAAGGCTGAACCTGGCTCAGACGTGGGTGAG
 CGGTAATGACCACAAAGGCAAGAAAAACCATGATCGTTTTTAGGTTGGC
 AGCCTGAAATCGTAGGAAATACATCAGAAATGTTACAAACAGG (SEQ ID NO:45)

amino acid sequence of drFP583

MRSSKNVIKEFMRFKVRMEGTVNNGHEFEIEEGEGRPYEGHNTVKLKVTKGGLPLFAWDILSPQFQ
 YGSKVYVKH PADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSD
 GPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLDGGHYLVEFKSIYMAKPVQLPGYYYYVDSK
 LDITSHNEDYTIVEQYERTEGRHHFL SEQ ID NO:012)

amino acid sequence of drFP583.1

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys
 Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu
 Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys
 Leu Lys Val Thr Lys Gly Pro Leu Pro Phe Ala Trp Asp Ile
 Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His
 Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly
 Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Val Val
 Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Cys Phe Ile Tyr
 Lys Ser Ser Leu Ala Leu Asn Phe Pro Ser Asp Gly Pro Val
 Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Leu
 Gly His Tyr Leu Val Glu Phe Lys Ser Ile Ile Met Ala Lys Lys
 Pro Val Gln Leu Pro Gly Tyr Tyr Val Asp Ser Lys Leu Asp
 Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu
 Arg Ser Glu Gly Arg His His Leu Phe Leu
 (SEQ ID NO:46)

FIGURE 7

Amino Acid and Nucleotide Sequence for asFP600

ATGGCTTCCTTTAAAGAAGACTATGCCCTTAAGACGACCATTGAAGGGACGGTTAATGGCCAC
TACTTCAAGTGTACAGGAAAAGGGAGGGCAACCCATTGAGGGTACGCAGGAATGAAGATAGAG
GTCATCGAAGGAGGTCCATTGCCATTGCCACATTGTCAACGAGTTATGTACGGTAGT
AAGGCCTTCATCAAGTATGTGTAGGAATTCTGACTACTCAAGCAGTCTTCCCTGAAGGTTT
ACTTGGGAAAGAACCAACCTACGAGGATGGAGGCTTCTTACAGCTCATCAGGACACAAGCCTA
GATGGAGATTGCCTCGTTACAAGGTCAAGATTCTGGTAATAATTTCCTGCTGATGGCCCCGTG
ATGCAGAACAAAGCAGGAAGATGGGAGGCCATCCACCGAGATAGTTATGAAGTTGACGGTGTCTG
CGTGGACAGTCTTGATGGCCCTTAAGTGCCCTGGTGGTCGTATCTGACTGCCATCTCCATACT
ACTTACAGGTCAAAAAACCAGCTGCTGCCTTGAAGATGCCAGGATTCAAGATCATCGC
ATCGAGATAATGGAGGAAGTTGAGAAAGGCAAGTGCTATAAACAGTACGAAGCAGCAGTGGCAGG
TACTGTGATGCTGCTCCATCCAAGCTTGGACATAAC (SEQ ID NO:13)

Amino acid

MASFLKKTMP FKTTIEGTVN GHYFKCTGKG EGNPFEGTQE MKIEVIEGGP LPFAFHILST
SCMYGSKTFI KYVSGIPDYF KQSFPEGFTW ERTTYEDGG FLTAHQDTSL DGDCLVYKV
ILGNNFPADG PVMQNKA GRW EPATEIVYEV DGVLRGQSLM ALKCPGGRHL TCHLHTTYRS
KKPAALKMP GFHFEDHRIE IMEEVEKGKC YKQYEAAVGR YCDAAPSKLG HN (SEQ ID
NO:14)

Figure 8

cDNA sequence of dgFP512

attcacacctg	gtgatttgt	a	agagaaagg	ta	caccatcaa	gagaagag	ct	gtaaaagtta	60					
atattttact	gtacttctac	c	cagcatg	gt	caactaaag	aagaatgaa	aatcaac	ctt	120					
acaatggaag	gtgttgtt	aa	cgggcttcc	t	taagatcc	gtgggatgg	aaaagg	caaa	180					
ccataccagg	gatcacag	g	ttaacctt	g	cggtgg	taaaggccc	tctgcctt	c	240					
tcttatgata	ttctgaca	ac	acatgttc	g	acggcaaca	gggcattc	gt	aaactaccc	300					
gaggacatac	cagatattt	ca	aggcagacc	t	ttctgg	ctaatgg	atattc	cgg	360					
caaaggacca	tgacttat	g	agacggagg	g	ttgcact	ctacaag	ca	catcagcgt	420					
gttggc	gaca	c	tttcaatta	t	gacattc	tttatgg	cg	aaatttcc	480					
ccagtgtgc	agaaaaga	a	aatgaaatgg	g	aaccatcc	ctgagata	at	tttgaacgt	540					
gatggaatgc	tgaggg	g	tgcatt	c	tctctgt	tgaagg	gg	ccattac	600					
cgatgtgatt	ttgaaactat	t	tataaacc	c	aataagg	tcaagat	cc	agattacc	660					
tttgtggacc	actgcatt	g	ataac	g	acaggatt	attacaac	gt	ggtttagct	720					
accgaggtt	ctgaagcc	c	ctact	ttcg	ctggag	tcggcaat	c	aaaggcgt	780					
atccaagcaa	tctaag	aa	aa	caacaagg	ca	ttaaacc	tcaccgt	ttt	gaat	tttcg	840			
ttcggaa	attt	c	ttggta	aa	aa	ctagg	ttt	cat	ttcg	ctgg	ac	ttctt	gact	900
cagctgt	aga	ca	agaa	ag	(SEQ ID NO:15)									919

amino acid sequence of dgFP512

Met Ser Ala Leu Lys Glu Glu Met Lys Ile Asn Leu Thr Met Glu
 Gly Val Val Asn Gly Leu Pro Phe Lys Ile Arg Gly Asp Gly Lys
 Gly Lys Pro Tyr Gln Gly Ser Gln Glu Leu Thr Leu Thr Val Val
 Lys Gly Gly Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Met
 Phe Gln Tyr Gly Asn Arg Ala Phe Val Asn Tyr Pro Glu Asp Ile
 Pro Asp Ile Phe Lys Gln Thr Cys Ser Gly Pro Asn Gly Gly Tyr
 Ser Trp Gln Arg Thr Met Thr Tyr Glu Asp Gly Gly Val Cys Thr
 Ala Thr Ser Asn Ile Ser Val Val Gly Asp Thr Phe Asn Tyr Asp
 Ile His Phe Met Gly Ala Asn Phe Pro Leu Asp Gly Pro Val Met
 Gln Lys Arg Thr Met Lys Trp Glu Pro Ser Thr Glu Ile Met Phe
 Glu Arg Asp Gly Met Leu Arg Gly Asp Ile Ala Met Ser Leu Leu
 Leu Lys Gly Gly His Tyr Arg Cys Asp Phe Glu Thr Ile Tyr
 Lys Pro Asn Lys Val Val Lys Met Pro Asp Tyr His Phe Val Asp
 His Cys Ile Glu Ile Thr Ser Gln Gln Asp Tyr Tyr Asn Val Val
 Glu Leu Thr Glu Val Ala Glu Ala Arg Tyr Ser Ser Leu Glu Lys
 Ile Gly Lys Ser Lys Ala
 (SEQ ID NO:16)

FIGURE 9

cDNA sequence of dmFP592

agtttcagcc agtgacaggg tgagctgcca ggtattctaa caagatgagt tggccaaga 60
 atgtgatcaa ggagttcatg aggttcaagg ttctgtatgga aggaacggc aatgggcacg 120
 agtttgaat aaaaggcgaa ggtgaaggga ggccttacga aggtcactgt tccgtaaagc 180
 ttatggtaac caagggtgga cctttccat ttgctttga tattttgtca ccacaatttc 240
 agtatggaag caaggtataat gtcaaacacc ctgccgacat accagactat aaaaagctgt 300
 catttcctga gggatttaaa tggaaagg tcataactt tgaagacggt ggcgtggta 360
 ctgtatccca agattccagt ttgaaagacg gctgtttcat ctacgaggc aagttcattg 420
 gggtgaactt tccttctgat ggacctgtt gtcagaggag gacacgggc tggaaagcca 480
 gctctgagcg tttgtatcct cgtgatgggg tgctgaaagg agacatccat atggctctga 540
 ggctggaagg aggccgcat tacctcggt aattcaaaag tatttacatg gtaaagaagc 600
 cttcagtgca gttgccaggc tactattatg ttgactccaa actggatatg acgagccaca 660
 acgaagatta cacagtcgtt gagcagtagt aaaaaaccca gggaccccac catccgttca 720
 ttaagcctct gcagtgaact cggctcagtc atggattagc ggtaatggcc acaaaaaggca 780
 cgatgatcgt ttttaggaa tgcagccaaa aattgaaggt tatgacagta gaaatacaag 840
 caacaggctt tgcttattaa acatgttaatt gaaaac 876

(SEQ ID NO:17)

amino acid sequence of dmFP592

Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys
 Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys
 Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys
 Leu Met Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile
 Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His
 Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly
 Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val
 Thr Val Ser Gln Asp Ser Ser Leu Lys Asp Gly Cys Phe Ile Tyr
 Glu Val Lys Phe Ile Gly Val Asn Phe Pro Ser Asp Gly Pro Val
 Met Gln Arg Arg Thr Arg Gly Trp Glu Ala Ser Ser Glu Arg Leu
 Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp Ile His Met Ala Leu
 Arg Leu Glu Gly Gly His Tyr Leu Val Glu Phe Lys Ser Ile
 Tyr Met Val Lys Lys Pro Ser Val Gln Leu Pro Gly Tyr Tyr Tyr
 Val Asp Ser Lys Leu Asp Met Thr Ser His Asn Glu Asp Tyr Thr
 Val Val Glu Gln Tyr Glu Lys Thr Gln Gly Arg His His Pro Phe
 Ile Lys Pro Leu Gln
 (SEQ ID NO:18)

Figure 10

	M	A	L	S	N	E	F	I	G	D	D	M	K	M	
676	ATG	GCC	CTG	TCC	AAC	GAG	TTC	ATC	GGC	GAC	GAC	ATG	AAG	ATG	
	TAC	CGG	GAC	AGG	TTG	TTC	AAG	TAG	CCG	CTG	CTG	TAC	TTC	TAC	
	T	Y	H	M	D	G	C	V	N	G	H	Y	F	T	V
721	ACC	TAC	CAC	ATG	GAC	GGC	TGC	GTG	AAC	GGC	CAC	TAC	TTC	ACC	GTG
	TGG	ATG	GTG	TAC	CTG	CCG	ACG	CAC	TTG	CCG	GTG	ATG	AAG	TGG	CAC
	K	G	E	G	S	G	K	P	Y	E	G	T	Q	T	S
766	AAG	GGC	GAG	GGC	AGC	GGC	AAG	CCC	TAC	GAG	GGC	ACC	CAG	ACC	TCC
	TTC	CCG	CTC	CCG	TCG	CCG	TTC	GGG	ATG	CTC	CCG	TGG	GTC	TGG	AGG
	T	F	K	V	T	M	A	N	G	G	P	L	A	F	S
811	ACC	TTC	AAG	GTG	ACC	ATG	GCC	AAC	GGC	GGC	CCC	CTG	GCC	TTC	TCC
	TGG	AAG	TTC	CAC	TGG	TAC	CGG	TTG	CCG	CCG	GGG	GAC	CGG	AAG	AGG
	F	D	I	L	S	T	V	F	M	Y	G	N	R	C	F
856	TTC	GAC	ATC	CTG	TCC	ACC	GTG	TTC	ATG	TAC	GGC	AAC	CGC	TGC	TTC
	AAG	CTG	TAG	GAC	AGG	TGG	CAC	AAG	TAC	ATG	CCG	TTG	GCG	ACG	AAG
	T	A	Y	P	T	S	M	P	D	Y	F	K	Q	A	F
901	ACC	GCC	TAC	CCC	ACC	AGC	ATG	CCC	GAC	TAC	TTC	AAG	CAG	GCC	TTC
	TGG	CGG	ATG	GGG	TGG	TCG	TAC	GGG	CTG	ATG	AAG	TTC	GTC	CGG	AAG
	P	D	G	M	S	Y	E	R	T	F	T	Y	E	D	G
946	CCC	GAC	GGC	ATG	TCC	TAC	GAG	AGA	ACC	TTC	ACC	TAC	GAG	GAC	GGC
	GGG	CTG	CCG	TAC	AGG	ATG	CTC	TCT	TGG	AAG	TGG	ATG	CTC	CTG	CCG
	G	V	A	T	A	S	W	E	I	S	L	K	G	N	C
991	GGC	GTG	GCC	ACC	GCC	AGC	TGG	GAG	ATC	AGC	CTG	AAG	GGC	AAC	TGC
	CCG	CAC	CGG	TGG	CGG	TCG	ACC	CTC	TAG	TCG	GAC	TTC	CCG	TTG	ACG
	F	E	H	K	S	T	F	H	G	V	N	F	P	A	D
1036	TTC	GAG	CAC	AAG	TCC	ACC	TTC	CAC	GGC	GTG	AAC	TTC	CCC	GCC	GAC
	AAG	CTC	GTG	TTC	AGG	TGG	AAG	GTG	CCG	CAC	TTG	AAG	GGG	CGG	CTG
	G	P	V	M	A	K	K	T	T	G	W	D	P	S	F
1081	GGC	CCC	GTG	ATG	GCC	AAG	AAG	ACC	ACC	GGC	TGG	GAC	CCC	TCC	TTC
	CCG	GGG	CAC	TAC	CGG	TTC	TTC	TGG	TGG	CCG	ACC	CTG	GGG	AGG	AAG
	E	K	M	T	V	C	D	G	I	L	K	G	D	V	T
1126	GAG	AAG	ATG	ACC	GTG	TGC	GAC	GGC	ATC	TTG	AAG	GGC	GAC	GTG	ACC
	CTC	TTC	TAC	TGG	CAC	ACG	CTG	CCG	TAG	AAC	TTC	CCG	CTG	CAC	TGG
	A	F	L	M	L	Q	G	G	G	N	Y	R	C	Q	F
1171	GCC	TTC	CTG	ATG	CTG	CAG	GGC	GGC	GGC	AAC	TAC	AGA	TGC	CAG	TTC
	CGG	AAG	GAC	TAC	GAC	GTC	CCG	CCG	CCG	TTG	ATG	TCT	ACG	GTC	AAG
	H	T	S	Y	K	T	K	K	P	V	T	M	P	P	N
1216	CAC	ACC	TCC	TAC	AAG	ACC	AAG	AAG	CCC	GTG	ACC	ATG	CCC	CCC	AAC
	GTG	TGG	AGG	ATG	TTC	TGG	TTC	TTC	GGG	CAC	TGG	TAC	GGG	GGG	TTG
	H	V	V	E	H	R	I	A	R	T	D	L	D	K	G
1261	CAC	GTG	GTG	GAG	CAC	CGC	ATC	GCC	AGA	ACC	GAC	CTG	GAC	AAG	GGC
	GTG	CAC	CAC	CTC	GTG	GCG	TAG	CGG	TCT	TGG	CTG	GAC	CTG	TTC	CCG
	G	N	S	V	Q	L	T	E	H	A	V	A	H	I	T
1306	GGC	AAC	AGC	GTG	CAG	CTG	ACC	GAG	CAC	GCC	GTG	GCC	CAC	ATC	ACC
	CCG	TTG	TCG	CAC	GTC	GAC	TGG	CTC	GTG	CGG	CAC	CGG	GTG	TAG	TGG
	S	V	V	P	F	*									
1351	TCC	GTG	GTG	CCC	TTC	TGA									
	AGG	CAC	CAC	GGG	AAG	ACT									

(SEQ ID NO:27 & 28)

Figure 11

Non-aggregating mutant FP3-NA was generated from zFP506-N65M (non-humanized version). In comparison with zFP506-N65M, FP3-NA contains two additional amino acid substitutions - K5E and K10E. Also, one accidental nucleotide substitution was introduced due to PCR mistake (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCT CAG TCA GAG CAC GGT CTA ACA GAA GAA ATG ACA ATG AAA
BamHI A Q S E H G L T E E M T M K

TAC CGT ATG GAA GGG TGC GTC GAT GGA CAT AAA TTT GTG ATC ACG GGA
Y R M E G C V D G H K F V I T G

GAG GGC ATT GGA TAT CCG TTC AAA GGG AAA CAG GCT ATT AAT CTG TGT
E G I G Y P F K G K Q A I N L C

GTG GTC GAA GGT GGA CCA TTG CCA TTT GCC GAA GAC ATA TTG TCA GCT
V V E G G P L P F A E D I L S A

GCC TTT ATG TAC GGA AAC AGG GTT TTC ACT GAA TAT CCT CAA GAC ATA
A F M Y G N R V F T E Y P Q D I

GTT GAC TAT TTC AAG AAC TCG TGT CCT GCT GGA TAT ACA TGG GAC AGG
V D Y F K N S C P A G Y T W D R

TCT TTT CTC TTT GAG GAT GGA GCA GTT TGC ATA TGT AAT GCA GAT ATA
S F L F E D G A V C I C N A D I

ACA GTG AGT GTT GAA GAA AAC TGC ATG TAT CAT GAG TCC AAA TTC TAT
T V S V E E N C M Y H E S K F Y

GGA GTG AAT TTT CCT GCT GAT GGA CCT GTG ATG AAA AAG ATG ACA GAT
G V N F P A D G P V M K K M T D

AAC TGG GAG CCA TCC TGC GAG AAG ATC ATA CCA GTA CCT AAG CAG GGG
N W E P S C E K I I P V P K Q G

ATA TTG AAA GGG GAT GTC TCC ATG TAC CTC CTT CTG AAG GAT GGT GGG
I L K G D V S M Y L L L K D G G

CGT TTA CGG TGC CAA TTC GAC ACA GTT TAC AAA GCA AAG TCT GTG CCA
R L R C Q F D T V Y K A K S V P

AGA AAG ATG CCG GAC TGG CAC TTC ATC CAG CAT AAG CTC ACC CGT GAA
R K M P D W H F I Q H K L T R E

GAC CGC AGC GAT GCT AAG AAT CAG AAA TGG CAT CTG ACA GAA CAT GCT
D R S D A K N Q K W H L T E H A

ATT GCA TCC GGA TCT GCA TTG CCC TGA AAGCTT
I A S G S A L P * HindIII (SEQ ID NO:29 & 30)

```

12/19

Figure 12

Amino acid sequence of zFP506 Yellow mutant

MAQSKHGLTKEMTMKYRMEGCVGDGHKFVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTYPEPQDI
VDYFKNSCPAGYTWDRSFLFEDGAVCICNADITVSVEENCMYHESKFYGVNFPADGPVMKKMDNWEPSCEKIIIPVPKQ
GILKGDVSMYLLLKDGGRLRCQFDTVYAKSVPRKMPDWHFIQHKLTRDRSDAKNQKWHLTEHAIASGSALP*
(SEQ ID NO:31)

Figure 13

Amino Acid Sequence of zFP506 Yellow/bright mutant

MAQSKHGLTKEMTMKYRMEGCVGDGHKFVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTYPEPQDI
VDYFKNSCPAGYTWNRSFLFEDGAVCICNADITVSVEENCVYHESKFYGVNFPADGPVMKKMDNWEPSCEKIIIPVPRQ
GILKGDVSMYLLLKDGGRLRCQFDTVYAKSVPRKMPDWHFIQHKLTRDRSDAKNQKWHLTEHAIASGSALS*
(SEQ ID NO:32)

Figure 14

Non-aggregating mutant FP4-NA was generated from zFP538-M128V (humanized version). In comparison with zFP538-M128V, FP4-NA contains two additional amino acid substitutions - K5E and K9T. Also, two accidental nucleotide substitutions were introduced due to PCR mistakes (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCC CAC AGC GAG CAC GGC CTG ACC GAG GAG ATG ACC ATG AAG
BamHI   A   H   S   E   H   G   L   T   E   E   M   T   M   K

TAC CAC ATG GAG GGC TGC GTG AAC GGC CAC AAG TTC GTG ATC ACC GGC
Y   H   M   E   G   C   V   N   G   H   K   F   V   I   T   G

GAG GGC ATC GGC TAC CCC TTC AAG GGC AAG CAG ACC ATC AAC CTG TGC
E   G   I   G   Y   P   F   K   G   K   Q   T   I   N   L   C

GTG ATC GAG GGC GGC CCC CTG CCC TTC AGC GAG GAC ATC CTG AGC GCC
V   I   E   G   G   P   L   P   F   S   E   D   I   L   S   A

GGC TTC AAG TAC GGC GAC CGG ATC TTC ACC GAG TAC CCC CAG GAC ATC
G   F   K   Y   G   D   R   I   F   T   E   Y   P   Q   D   I

GTG GAC TAC TTC AAG AAC AGC TGC CCC GCC GGC TAC ACC TGG GGC CGG
V   D   Y   F   K   N   S   C   P   A   G   Y   T   W   G   R

AGC TTC CTG TTC GAG GAC GGC GCC GTG TGC ATC TGT AAC GTG GAC ATC
S   F   L   F   E   D   G   A   V   C   I   C   N   V   D   I

ACC GTG AGC GTG AAG GAG AAC TGC ATC TAC CAC AAG AGC ATC TTC AAC
T   V   S   V   K   E   N   C   I   Y   H   K   S   I   F   N

GGC GTG AAC TTC CCC GCC GAC GGC CCC GTG ATG AAG AAG ATG ACC ACC
G   V   N   F   P   A   D   G   P   V   M   K   K   M   T   T

AAC TGG GAG GCC AGC TGC GAG AAG ATC ATG CCC GTG CCT AAG CAG GGC
N   W   E   A   S   C   E   K   I   M   P   V   P   K   Q   G

ATC CTG AAG GGC GAC GTG AGC ATG TAC CTG CTG CTG AAG GAC GGC GGC
I   L   K   G   D   V   S   M   Y   L   L   L   K   D   G   G

CGG TAC CGG TGC CAG TTC GAC ACC GTG TAC AAG GCC AAG AGC GTG CCC
R   Y   R   C   Q   F   D   T   V   Y   K   A   K   S   V   P

AGC AAG ATG CCC GAG TGG CAC TTC ATC CAG CAC AAG CTG CTG CGG GAG
S   K   M   P   E   W   H   F   I   Q   H   K   L   L   R   E

GAC CGG AGC GAC GCC AAG AAC CAG AAG TGG CAG CTG ACC GAG CAC GCC
D   R   S   D   A   K   N   Q   K   W   Q   L   T   E   H   A

ATC GCC TTC CCC AGC GCC CTG GCC TGA AAGCTT
I   A   F   P   S   A   L   A   * HindIII      (SEQ ID NOS: 33-34)

```

Figure 15

All mutants are derived from drFP583 (called "pink" or FP6.) by random mutagenesis

The mutants E57 and AG4 are derivative from E5

Mutant: E5 = V105A, S197T Phenotype: in *E.coli* seen as Green overnight, matures

to Red over 24h at 37°C (final peaks ratio Red vs. Green is 75:25); folding is faster than FP6.

Mutant: E8 = N42H Phenotype: always has two peaks Green & Red in approx. 60:40; folding is faster than E5 (about 8h at 37°C)

Mutant: E83 = N42H, V71A, I180V Phenotype: always has two almost equal peaks Green & Red; folding is the same as for E8

Mutant: E5up = V105A Phenotype: seen as Red from the beginning; folding is faster than E5 (about 12-16h) Almost no Green peak at final point of maturation

Mutant: E57 = V105A, I161T, S197A Phenotype: at common is like E5up but folding is more faster (no more than 8-10h) Very small Green peak at final point of maturation (less than 5%)

Mutant: E5down = S197T Phenotype and folding rate are exactly the same as for E5

Mutant: AG4 = V71M, V105A, S197T Phenotype: Very bright Green, no Red at all (even at the beginning); folding is faster than E5 (no more than 16h)

Mutant: AG4 = V71M, V105A, Y120H, S197T Phenotype: at common is like AG4, but more brighter (approx. twice) one.

1	Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val	16
1	ATG CGC TCC TCC AAG AAC GTC ATC AAG GAG TTC ATG CGC TTC AAG GTG	48
17	Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu	32
49	CGC ATG GAG GGC ACC GTG AAC GGC CAC GAG TTC GAG ATC GAG GGC GAG	96
	His (CAC) for E8 and E83	
33	Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val	48
97	GGC GAG GGC CGC CCC TAC GAG GGC CAC <u>AAC</u> ACC GTG AAG CTG AAG GTG	144
49	Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln	64
145	ACC AAG GGC GGC CCC CTG CCC TTC GCC TGG GAC ATC CTG TCC CCC CAG	192
	Met (ATG) for AG4 and AG45/Ala(GCG) for E83	
65	Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro	80
193	TTC CAG TAC GGC TCC AAG <u>GTG</u> TAC GTG AAG CAC CCC GCC GAC ATC CCC	240
81	Asp Tyr Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val	96
241	GAC TAC AAG CTG TCC CCC GAG GGC TTC AAG TGG GAG CGC GTG	288
	Ala (GCG)-for E5, E57, AG4 and AG45	
97	Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser	112
289	ATG AAC TTC GAG GAC GGC GGC <u>GTG</u> ACC GTG ACC CAG GAC TCC TCC	336
	His (CAC) -for AG45	
113	Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn	128
337	CTG CAG GAC GGC TGC TTC ATC <u>TAC</u> AAG GTG AAG TTC ATC GGC GTG AAC	384
129	Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu	144
385	TTC CCC TCC GAC GGC CCC GTG ATG CAG AAG ACC ATG GGC TGG GAG	432
145	Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu	160
433	GCC TCC ACC GAG CGC CTG TAC CCC CGC GAC GGC GTG CTG AAG GGC GAG	480
	Thr (ACC) for E57	
161	Ile His Lys Ala Leu Lys Asp Gly Gly His Tyr Leu Val Glu	176
481	<u>ATC</u> CAC AAG GCC CTG AAG GAC GGC CAC TAC CTG GTG GAG	528
	Val (GTC) for E83	
177	Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr	192
529	TTC AAG TCC <u>ATC</u> TAC ATG GCC AAG CCC GTG CAG CTG CCC GGC TAC	576
	Thr (ACC) for E5, AG4 and AG45/Ala(GCC) for E57	
193	Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr	208
577	TAC TAC GTG GAC <u>TCC</u> AAG CTG GAC ATC ACC TCC CAC AAC GAG GAC TAC	624
209	Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu ***	229
625	ACC ATC GTG GAG CAG TAC GAG CGC ACC GAG GGC CGC CAC CAC CTG TTC CTG TAA	678
	(SEQ ID NO:11 & 12)	

FIGURE 16

Nucleic acid sequence of humanized drFP583

ATGGTGCCTCCTCCAAGAACGTCAAGGAGTTCATGCGCTTCAAGGTGCGCATGG
 AGGGCACCGTGAACGGCCACGAGTCAGATCGAGGGCGAGGGCGAGGGCCGCC
 TACGAGGGCCACAACACCGTGAAGCTGAAGGTGACCAAGGGCGCCCTGCCCTC
 GCCTGGGACATCCTGTCCCCCAGTCCAGTACGGCTCCAAGGTGTACGTGAAGCACC
 CCGCCGACATCCCCACTACAAGAAGCTGTCCCTCCCCGAGGGCTTCAAGTGGGAGC
 GCGTGATGAACTTCGAGGACGGCGGTGGTACCGTGACCCAAGACTCCTCCCTGC
 AGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGCGTGAACCTCCCCTCCGACGG
 CCCCCTAATGCAGAAGAACCATGGGCTGGGAGGCCTCACCAGCGCCTGTACCC
 CCGCGACGGCGTGTGAAGGGCGAGATCCACAAGGCCTGAAGCTGAAGGACGGCG
 GCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGAACGCCCCTGCAGCTGCC
 CGGCTACTACTACGTGGACTCCAAGCTGGACATCACCTCCCACAACGAGGACTACAC
 CATCGTGGAGCAGTACGAGCGCACCGAGGGCCACCACCTGTTCTGTAG (SEQ ID
 NO:35)

Figure 17

DNA sequence (ORF) of E5-NA

ATGGCCTCCCGAGAACGTCACTACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGGCCACGAGT
 TCGAGATCGAGGGCGAGGGCGAGGGCCACACCCCTACGAGGGCACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCC
 CCTGCCCTTCGCTGGGACATCCTGTCCCCCAGTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATC
 CCCGACTACAAGAACGCTGTCTTCCCCAGGGCTTCAAGTGGAGCGCGTGAACTTCGAGGACGGCGGTGGCGA
 CCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTCATCTACAAGGTGAAGTTCATCGCGTGAACTTCCCCTCCGA
 CGGCCCCGTGATGCAGAAGAACATGGGCTGGGAGGCCTCACCAGCGCCTGTACCCCCCGCACGGCGTGTGAAG
 GGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCGCACTACCTGGTGGAGTTCAAGTCCATCTACATGCCAAGA
 AGCCCCGTGCAGCTGCCCGCTACTACTACGTGGACACCAAGCTGGACATCACCTCCCACAACGAGGACTACACCACGT
 GGAGCAGTACGAGCGCACCGAGGGCCACCACCTGTTCTGTAA (SEQ ID NO:36)

Figure 18

ATGGTGCCT CCTCCAAGAA CGTCATCAAG GAGTTCATGC GCTTCAAGGT
 GCGCATGGAGGGCACCGTGA ACGGCCACGA GTTCGAGATC GAGGGCGAGG GCGAGGGCCG
 CCCCTACGAG GGCCACAACA CCGTGAAGCT GAAGGTGACC AAGGGCGGCC CCCTGCCCT
 CGCCTGGGAC ATCCTGTCCC CCCAGTTCCA GTACGGCTCC AAGGTGTACG TGAAGCACCC
 CGCCGACATC CCCGACTACA AGAAGCTGTC CTTCCCCGAG GGCTCAAGT GGGAGCGCGT
 GATGAACCTCGAGGACGGCG GCGTGGCGAC CGTGAACCAA GACTCCTCCC TGCAAGGACGG
 CTGCTTCATC TACAAGGTGA AGTTCATCGG CGTGAACCTC CCCTCCGACG GCCCCGTAAT
 GCAGAAGAACCATGGGCT GGGAGGCCTC CACCGAGCGC CTGTACCCCCC GCGACGGCGT
 GCTGAAGGGC GAGACCCACA AGGCCCTGAA GCTGAAGGAC GGCGGCCACT ACCTGGTGG
 GTTCAAGTCC ATCTACATGG CCAAGAACGC CGTGCAGCTG CCCGGCTACT ACTACGTGGA
 CGCCAAGCTG GACATCACCT CCCACAACGA GGACTACACC ATCGTGGAGC AGTACGAGCG
 CACCGAGGGCCGCCACCACCGTGTAA G (SEQ ID NO:37)

Figure 19.

Nucleic acid sequence FP6 (E57)-NA

ATGGCCTCCGAGAACGTCATACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGA
ACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCTACGAGGGCCACAACACCGTG
AAGCTGAAGGTGACCAAGGGCGCCCCCTGCCCTCGCCTGGACATCCTGTCCCCCCCAGTCCAGT
ACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCGACTACAAGAAGCTGTCTTCCCCGA
GGGCTTCAAGTGGGAGCGCGTGTGAACCTCGAGGACGGCGGTGGGACCGTGACCCAGGACTC
CTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAACCTCCCCCTCCGACGGC
CCCGTGATGCAAGAAGAACATGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGGACGGC
GTGCTGAAGGGCGAGACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACTGGTGGAGTTC
AAGTCCATCTACATGGCCAAGAACGCCGTGCAGCTGCCGGCTACTACTACGTGGACGCCAGCTGG
ACATCACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCA
CCTGTTCTG (SEQ ID NO:38)

Figure 20.

Non-aggregating mutant FP7-NA was generated from M35-5 (FP7a). In comparison with M35-5, FP7-NA contains two additional substitutions - K6T and K7E. Nucleotide substitutions in the codon for Leu-4 were introduced to optimize codon usage (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCC TCC CTG CTG ACC GAG ACC ATG CCC TTC AGG ACC ACC ATC
BamHI   A     S     L     L     T     E     T     M     P     F     R     T     T     I

GAG GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG
E   G   T   V   N   G   H   Y   F   K   C   T   G   K   G   E

GGC AAC CCC CTC GAG GGC ACC CAG GAG ATG AAG ATC GAG GTG ATC GAG
G   N   P   L   E   G   T   Q   E   M   K   I   E   V   I   E

GGC GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG
G   G   P   L   P   F   A   F   H   I   L   S   T   S   C   M

TAC GGC TCC AAG GCC TTC ATC AAG TAC GTG TCC GGC ATC CCC GAC TAC
Y   G   S   K   A   F   I   K   Y   V   S   G   I   P   D   Y

TTC AAG CAG TCC CTC CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC
F   K   Q   S   L   P   E   G   F   T   W   E   R   T   T   T

TAC GAG GAC GGC GGC TTC CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC
Y   E   D   G   G   F   L   T   A   H   Q   D   T   S   L   D

GGC GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC
G   D   C   L   V   Y   K   V   K   I   L   G   N   N   F   P

GCC GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC
A   D   G   P   V   M   Q   N   K   A   G   R   W   E   P   S

ACC GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG
T   E   I   V   Y   E   V   D   G   V   L   R   G   Q   S   L

ATG GCC CTG GAG TGC CCC GGC GGT CGC CAC CTG ACC TGC CAC CTG CAC
M   A   L   E   C   P   G   G   R   H   L   T   C   H   L   H

ACC ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC
T   T   Y   R   S   K   K   P   A   S   A   L   K   M   P   G

TTC CAC TTC GAG GAC CAC CGC ATC GAG ATC CTG GAG GAG GTG GAG AAG
F   H   F   E   D   H   R   I   E   I   L   E   E   V   E   K

GGC AAG TGC TAC AAG CAG TAC GAG GGC GCC GGC GTG GGC CGC TAC TGC GAC
G   K   C   Y   K   Q   Y   E   A   A   V   G   R   Y   C   D

GCC GCC CCC TCC AAG CTG GGC CAC AAC TGAAGCTT
A   A   P   S   K   L   G   H   N   * HindIII (SEQ ID NO:39 & 40)

```

FIGURE 21

ATG GCC TCC **TTC** CTG AAG AAG **ACC** ATG CCC TTC **AAG** ACC ACC ATC GAG
 M A S F L K K T M P F K T T I E

 GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG GGC
 G T V N G H Y F K C T G K G E G

 AAC CCC **TTC** GAG GGC ACC CAG GAG ATG **AAG** ATC GAG GTG ATC GAG GGC
 N P F E G T Q E M K I E V I E G

 GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG TAC
 G P L P F A F H I L S T S C M Y

 GGC TCC AAG GCC TTC ATC AAG TAC **GTG** TCC GGC ATC CCC GAC TAC TTC
 G S K A F I K Y V S G I P D Y F

 AAG CAG TCC **TTC** CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC TAC
 K Q S F P E G F T W E R T T T Y

 GAG GAC GGC GGC **TTC** CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC GGC
 E D G G F L T A H Q D T S L D G

 GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC GCC
 D C L V Y K V K I L G N N F P A

 GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC ACC
 D G P V M Q N K A G R W E P S T

 GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG ATG
 E I V Y E V D G V L R G Q S L M

 GCC CTG **AAG** TGC CCC GGC GGC CGC CAC CTG ACC TGC CAC CTG CAC ACC
 A L K C P G G R H L T C H L H T

 ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC TTC
 T Y R S K K P A S A L K M P G F

 CAC TTC GAG GAC CAC CGC ATC GAG ATC **ATG** GAG GAG GTG GAG AAG GGC
 H F E D H R I E I M E E V E K G

 AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC **GAC** GCC
 K C Y K Q Y E A A V G R Y C D A

 GCC CCC TCC AAG CTG GGC CAC AAC TGA
 A P S K L G H N * (SEQ ID NO:41 & 42)

Figure 22

Sequence of humanized 6/9 hybrid gene and 6/9-Q3 mutant for 6/9-2G and 6/9-Q3 CAG(Q)																		
1	ATG	AGC	TGC	AGC	AAG	AAC	GTG	ATC	AAG	GAG	TTC	ATG	CGG	TTC	AAG	GTG		48
1	M	S	C	S	K	N	V	I	K	E	F	M	R	F	<u>K</u>	V		16
49	CGG	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	GAG	TTC	GAG	ATC	AAG	GGC	GAG		96
17	R	M	E	G	T	V	N	G	H	E	F	E	I	K	G	E		32
97	GGC	GAG	GGC	CGG	CCC	TAC	GAG	GGC	CAC	TGC	AGC	GTG	AAG	CTC	ATG	GTG		144
33	G	E	G	R	P	Y	E	G	H	C	S	V	K	L	M	V		48
145	ACC	AAG	GGC	GGC	CCC	CTC	CCC	TTC	GCC	TTC	GAC	ATC	CTC	AGC	CCC	CAG		192
49	T	K	G	G	P	L	P	F	A	F	D	I	L	S	P	Q		64
193	TTC	CAG	TAC	GGC	AGC	AAG	GTG	TAC	GTG	AAG	CAC	CCC	GCC	GAC	ATC	CCC		240
65	F	Q	Y	G	S	K	V	Y	V	K	H	P	A	D	I	P		80
ATG(M) for 6/9-Q3																		
241	GAC	TAC	AAG	AAG	CTC	AGC	TTC	CCC	GAG	GGC	TTC	AAG	TGG	GAG	CGG	GTG		288
81	D	Y	<u>K</u>	K	L	S	F	P	E	G	F	K	W	E	R	V		96
289	ATG	AAC	TTC	GAG	GAC	GGC	GGC	GTG	GTG	ACC	GTG	AGC	CAG	GAC	AGC	AGC		336
97	M	N	F	E	D	G	G	V	V	T	V	S	Q	D	S	S		112
337	CTC	AAG	GAC	GGC	TGC	TTC	ATC	TAC	GAG	GTG	AAG	TTC	ATC	GGC	GTG	AAC		384
113	L	K	D	G	C	F	I	Y	E	V	K	F	I	G	V	N		128
385	TTC	CCC	AGC	GAC	GGC	CCC	GTG	ATG	CAG	CGG	CGG	ACC	CGG	GGC	TGG	GAG		432
129	F	P	S	D	G	P	V	M	Q	R	R	T	R	G	W	E		144
433	GCC	AGC	AGC	GAG	CGG	CTC	TAC	CCC	CGG	GAC	GGC	GTG	CTC	AAG	GGC	GAC		480
145	A	S	S	E	R	L	Y	P	R	D	G	V	L	K	G	D		160
481	ATC	CAC	ATG	GCC	CTC	CGG	CTC	GAG	GGC	GGC	GGC	CAC	TAC	CTC	GTG	GAG		528
161	I	H	M	A	L	R	L	E	G	G	G	H	Y	L	V	E		176
529	TTC	AAG	AGC	ATC	TAC	ATG	GCC	AAG	AAG	CCC	GTG	CAG	CTC	CCC	GGC	TAC		576
177	F	K	S	I	Y	M	A	K	K	P	V	Q	L	P	G	Y		192
577	TAC	TAC	GTG	GAC	AGC	AAG	CTC	GAC	ATC	ACC	AGC	CAC	AAC	GAG	GAC	TAC		624
193	Y	Y	V	D	S	K	L	D	I	T	S	H	N	E	D	Y		208
TCC(S) for 6/9-2G and 6/9-Q3																		
625	ACC	ATC	GTG	GAG	CAG	TAC	GAG	CGG	ACC	GAG	GGC	CGG	CAC	CAC	CTC	TTC		672
209	T	I	V	E	Q	Y	E	R	<u>T</u>	E	G	R	H	H	L	F		224
673	CTC	TGA																678
225	L	*																226

(SEQ ID NO:43 & 44)